RAW SEQUENCE LISTING      DATE: 04/02/2001
PATENT APPLICATION: **US/09/020,743**      TIME: 14:23:25

Input Set : **A:\18547348.app**
Output Set: **N:\CRF3\04022001\I020743.raw**

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SEQUENCE LISTING
4 (1) GENERAL INFORMATION:
6    (i) APPLICANT: Mack, David H.
8   (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
9                          EXPRESSION COMPARISON
11  (iii) NUMBER OF SEQUENCES: 2
13   (iv) CORRESPONDENCE ADDRESS:
14        (A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
15                   Crew LLP
16        (B) STREET: Two Embarcadero Center, Eighth Floor
17        (C) CITY: San Francisco
18        (D) STATE: CA
19        (E) COUNTRY: USA
20        (F) ZIP: 94111-3834
22    (v) COMPUTER READABLE FORM:
23        (A) MEDIUM TYPE: Floppy disk
24        (B) COMPUTER: IBM PC compatible
25        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28   (vi) CURRENT APPLICATION DATA: `
C--> 29        **(A) APPLICATION NUMBER: US/09/020,743**
C--> 30        **(B) FILING DATE: 09-Feb-1998**
31        (C) CLASSIFICATION:
33  (viii) ATTORNEY/AGENT INFORMATION:
34        (A) NAME: Liebeschuetz, Joe
35        (B) REGISTRATION NUMBER: 37,505
36        (C) REFERENCE/DOCKET NUMBER: 018547034800US
38   (ix) TELECOMMUNICATION INFORMATION:
39        (A) TELEPHONE: (650) 326-2400
40        (B) TELEFAX: (650) 326-2422
43 (2) INFORMATION FOR SEQ ID NO: 1:
45    (i) SEQUENCE CHARACTERISTICS:
46        (A) LENGTH: 2691 base pairs
47        (B) TYPE: nucleic acid
48        (C) STRANDEDNESS: unknown
W--> 49        **(D) TOPOLOGY: not relevant**
51   (ii) MOLECULE TYPE: DNA (genomic)
53   (vi) ORIGINAL SOURCE:
54        (A) ORGANISM: Homo sapiens
58   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT      60
62 CATGGCTGAG TGAGCCTCCC CTGGGCCCAG CACCCCACCT CAGCATGGTC CAAGCCCATG     120
64 GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC     180
66 CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG     240
68 TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA     300
70 CACCCCGGGA GGTCACCCTA CACTTTCTGC GCACTGCTGG ACACCCCCTT ACCCGCTGGG     360
72 CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT     420

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 74 CAAACTTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA    480
 76 AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG    540
 78 ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA    600
 80 TTGCCACCCA GGGCCCCATG CCCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG    660
 82 AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC    720
 84 ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA    780
 86 AAGAGTGCCC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT    840
 88 CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC    900
 90 CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC    960
 92 CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA   1020
 94 TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC   1080
 96 TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA   1140
 98 CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT   1200
100 CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA   1260
102 AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG   1320
104 CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG   1380
106 CATTTATGAC AGACAAAGAA AGAAGCCCAG GTGTCCTGGT GTTCTCTGAG ACACTCTTTG   1440
108 TGAGCTTCAG TTTCCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA   1500
110 GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG   1560
112 TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCCAAGC ACAGGCCAGA TGCAAGAATG   1620
114 GGGAAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA   1680
116 CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC   1740
118 CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG   1800
120 AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC   1860
122 CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT   1920
124 TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT   1980
126 GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG   2040
128 ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT   2100
130 CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG   2160
132 CCACACCTCA GGATTCCTCC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA   2220
134 TGAAGGTAAG ATGCCGCATC ACCAGGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT   2280
136 CTCTGTGGAA ACCCCGAGG AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC   2340
138 TTCTCTCCTG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT   2400
140 GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC   2460
142 ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC   2520
144 TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG   2580
146 CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA   2640
148 GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C            2691
150 (2) INFORMATION FOR SEQ ID NO: 2:
152      (i) SEQUENCE CHARACTERISTICS:
153           (A) LENGTH: 360 amino acids
154           (B) TYPE: amino acid
155           (C) STRANDEDNESS: not relevant
156           (D) TOPOLOGY: not relevant
158      (ii) MOLECULE TYPE: protein
160      (vi) ORIGINAL SOURCE:
161           (A) ORGANISM: Homo sapiens
165      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
167      Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
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W--> 156

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168    1                 5                 10                15
170    Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Pro Glu Lys Thr Pro Ala
171              20                25                30
173    Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
174              35                40                45
176    Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
177              50                55                60
179    Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
180    65                70                75                80
182    Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
183              85                90                95
185    Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
186              100               105               110
188    Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
189              115               120               125
191    Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
192              130               135               140
194    Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
195    145               150               155               160
197    Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
198              165               170               175
200    Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
201              180               185               190
203    Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
204              195               200               205
206    Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
207              210               215               220
209    Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
210    225               230               235               240
212    Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
213              245               250               255
215    Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
216              260               265               270
218    Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
219              275               280               285
221    Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr
222              290               295               300
224    Arg Ile Gly Cys Gln Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu
225    305               310               315               320
227    Gly Ile Val Cys Gln Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr
228              325               330               335
230    Asp Glu Gln Tyr Gln Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly
231              340               345               350
233    Gln Leu Pro Glu Glu Pro Ser Pro
234              355               360
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**VERIFICATION SUMMARY**                    DATE: 04/02/2001
PATENT APPLICATION:   US/09/020,743         TIME: 14:23:26

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2